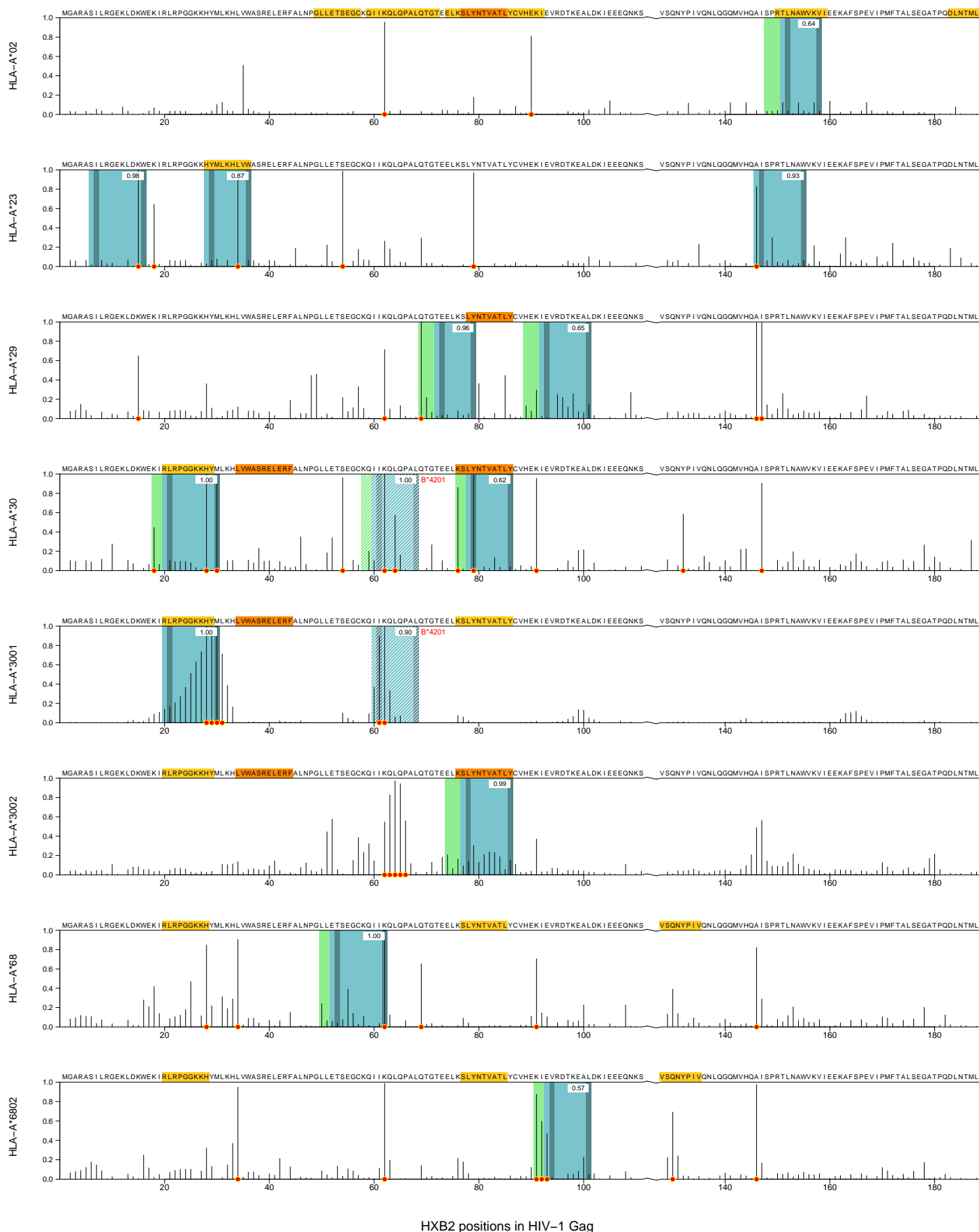
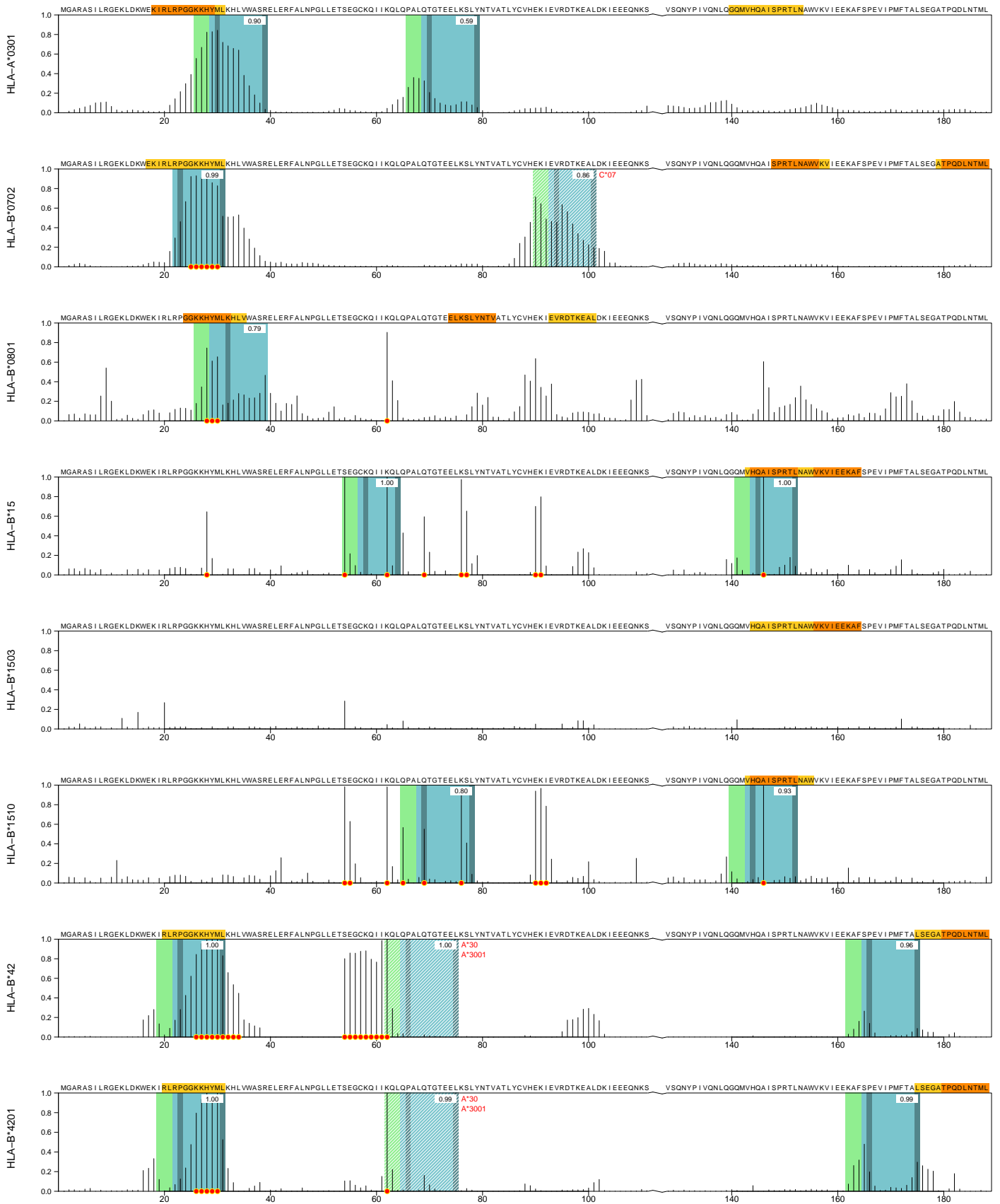
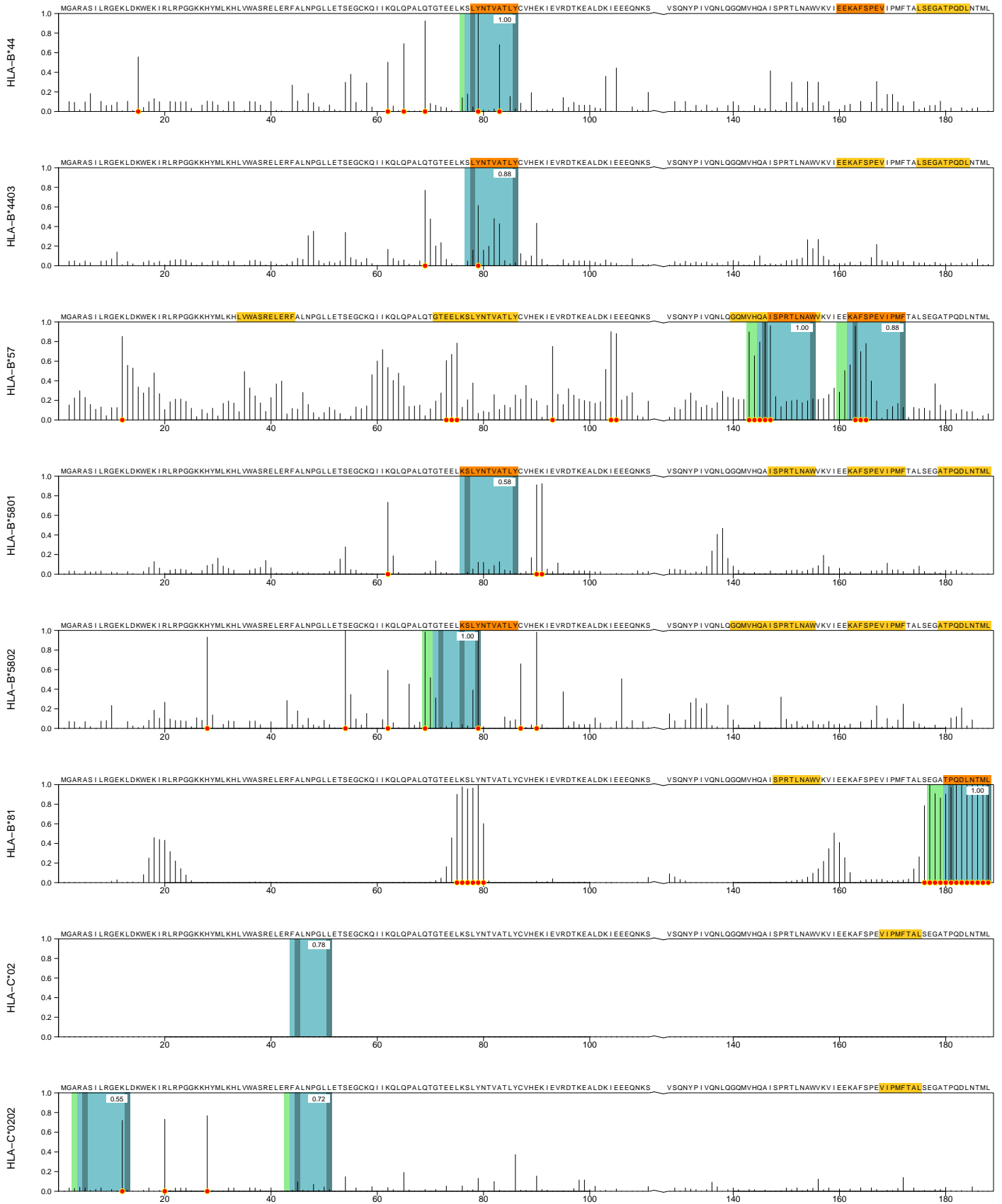


FIG. S1.—Posterior probabilities of the epitope state in HIV-1 Gag (HXB2 positions 1 to 188) based on the two-state epitope model. Light blue shaded regions indicate epitopes predicted by Viterbi decoding of the phylo-HMMwD+M with the posterior probability of each epitope given on the top right-hand corner. Predicted anchors are shaded in dark blue and flanking regions are shaded in green. Potentially spurious predictions that may have arisen due to HLA linkage disequilibrium are shaded with white stripes and the correlated HLA alleles to which such predictions may be attributed are indicated with red text. Red dots identify epitopes predicted by Viterbi decoding of the two-state model. Dark orange segments indicate best-defined or “A-list” epitopes, while light orange segments indicate other CTL epitopes described in Yusim et al. (2009).

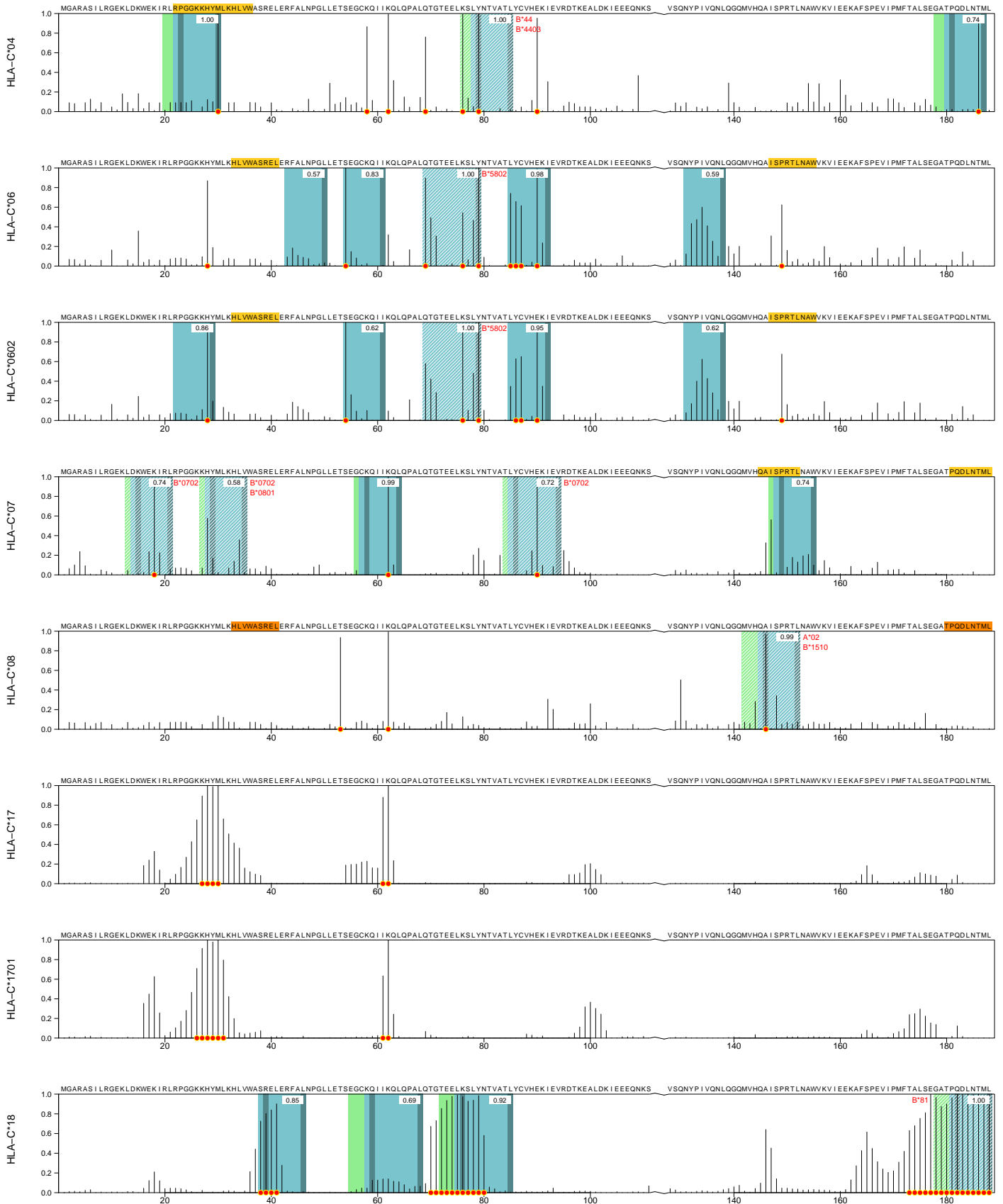




HXB2 positions in HIV-1 Gag



HXB2 positions in HIV-1 Gag



HXB2 positions in HIV-1 Gag